

Cystine-Knot Polypeptides: Cloaked-2 Molecules and Uses Thereof

Inventors: Paszty et al.

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Sheet 1 of 4 (Fig. 1)

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Figure 1

A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

```
1 TACTGGAAGGTGGCGTGCCTCCTCTGGCTGGTACCATGCAGCTCCACT
51 GGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCGGTGTAGTGG
101 AGGGCAGGGGTGGCAGGCTTCAAGAAATGATGCCACGAAATCATCCCC
151 GAGCTCGGAGAGTACCCCGAGCCTCCACCCGGAGCTGGAGAACAAAGAC
201 CATGAACCAGGGCGGAGAACCGAGGGCGGCCCTCCCACCCACCCCTTGAGA
251 CAAAGACGTGTCCGAGTACAGCTGCCCGAGCTGCACCTCACCCGCTAC
301 GTGACCGATGGGCCGTGCCGCAGGCCAACGCCATGGCCGCG
351 CTCCGCCAGTGCAGGCCGGCGCGCTGCTGCCAACGCCATGGCCGCG
401 GCAAGTGGTGGCGACCTAGTGGGCCGACTTCGCTGCATCCCCGACCGC
451 TACCGCGCGCAGCGCGTGCAGCTGCTGTCTCCGGTGGTGAGGCGCCGCG
501 CCGCGCAAGGTGCGCCTGGCTCGTCAAGTGCAGTGCAAGGCGCTCACCC
551 GCTTCACAACCAAGCTCGGAGCTCAAGGACTTCCGGACCGAGGGCGCTCGG
601 CCGCAGAAGGGCGGAGGCCGGCGCCCGCGAGCGCCAAGCCAA
651 CCAGGGCGAGCTGGAGAACGCCTAGAGCCCGCCCGGCCCTCCCCA
701 CCGGCGGGCGCCCCGGCCCTGAACCCGCGCCCCACATTCTGCTCTGC
751 GCGTGGTTT
```

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

```
1 QGWQAFKNDATEIIIPELGEYPEPPPELENNKTMNRAENGGRPPHHFETK
51 DVSEYSCRELHFTRYVTDGPCRSAPVTELVCSQCGPARLLPNAIGRK
101 WWRPSGPDFRCIPDRYRAQRVQLLCPGEAPRARKVRLVASCKCKRLTRF
151 HNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAY
```

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

```
1 MQLPLALCLVCLLVHTAFRVVEQGWQAFKNDATEIIIPELGEYPEPPPEL
51 ENNKTMNRAENGGRPPHHFETKDVSEYSCRELHFTRYVTDGPCRSAPV
101 TELVCSGQCGPALLPNAIGRGKWWRPSGPDFRCIPDRYRAQRVQLLCP
151 GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR
201 SAKANQAELENAY
```

Figure 2

A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

1 **ATGCAGCCCTCACTAGCCCCGTGCCCATCTGCCTACTTGTGCACGCTGC**
51 **CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA**
101 **CAGAGGTCACTCCAGGGCTTGAGAGTACCCCGAGCCTCTTGAGAAC**
151 **AACCAGACCATGAACCGGGCGAGAAATGGAGGCAGACCTCCCCACCATCC**
201 **CTATGACGCCAAAGATGTGTCGAGTACAGCTGCCCGAGCTGCACATACA**
251 **CCCGCTTCTGACAGACGGCCCAGTGCCCGAGCGCCAAGCCGGTCACCGAG**
301 **TTGGGTGCTCCGCCAGTGCAGGCCCGCGCGCTGCTGCCAACGCCAT**
351 **CGGGCGCGTGAAGTGGTGGCCCGAACCGGACCGGATTTCGCTGCATCC**
401 **CGGATCGCTACCGCGCGAGCGGGTGCAGCTGCTGTGCCCCGGGGCGCG**
451 **GCGCCCGCCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAGTGCAGCG**
501 **CCTCACCCGCTTCACAACCAAGTCGGAGCTCAAGGACTTCGGGGAGA**
551 **CCGCGCGGCCGAGAAGGGTCGCAAGCCGCCGGCGCCCCGGAGCC**
601 **AAAGCCAACCAGGCGGAGCTGGAGAACGCCCTACTAG**

B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

1 QGWQAFRNDATEVIPGLGEYPEPPPENNQTMNRAENGGRPPHHPYDAKDV
51 SEYS**CRELHYTRFLTDGP**CRSAKPVTELVC**SGQCGPARLLPNAIGRVKWW**
101 RPNGPDFRCI**PDRYRAQRVQLLC**PGGAAPRSRKVRLVAS**CKCKRLTRFHN**
151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY

C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

1 MQPSLAPCLICLLVHA~~AFC~~CAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
51 NQTMNRAENGGRPPHHPYDAKDVSEYS**CRELHYTRFLTDGP**CRSAKPVTE
101 LV**CSGQCGPARLLPNAIGRVKWW**RPNPDFRCI**PDRYRAQRVQLLC**PGGA
151 APRSRKVRLVAS**CKCKRLTRFHN**QSELKDFGPETARPQKGRKPRPGARGA
201 KANQAELENAY

Figure 3

GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213
to: Mouse Cloaked-2 check: 9489 from: 1 to: 211

Symbol comparison table:
/GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 8 Average Match: 2.912
 Length Weight: 2 Average Mismatch: -2.003
 Quality: 1028 Length: 213
 Ratio: 4.872 Gaps: 1
 Percent Similarity: 91.469 Percent Identity: 88.152

```
Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1
```

Human Cloaked-2 (SEQ ID NO: 5) x
Mouse Cloaked-2 (SEQ ID NO: 6)

Figure 4

GAP of: Human Cloaked-1 check: 1888 from: 1 to: 183
to: Human Cloaked-2 check: 185 from: 1 to: 190

Symbol comparison table:
/GCGDISK/gcg10/gcgccore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003
Quality:	335	Length:	196
Ratio:	1.831	Gaps:	6
Percent Similarity:	52.542	Percent Identity:	42.938

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

Human Cloaked-1 (SEQ ID NO: 25) x
Human Cloaked-2 (SEQ ID NO: 2)

1FKNDATEILYSHVVVP.VPAHPSSNSTLNRQARNGGRHFSNTGLDR	44
	: : . : . . :	
1	QGWQAFKNDATEIIPELGEYPEPPPPELENNKTMNRAENGGRP.PHHPFET	49
45	NTRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGGG	94
	: : : . . : .	
50	KDVSEYSCRELHFTRYVTDGP <u>CrsAKPVTELVC</u> SGQCGPARLLPNAIGRG	99
95	YGTKYWSRRSSQEWR <u>CvNDKTRTQR</u> IQLQCQDG.SRTTYKITVVTACKCK	143
	: : . : : : . : . .	
100	...KWW.RPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVAS <u>C</u> CKCK	145
144	RYTRQHNESSHNFE <u>MSPAKPVQHH</u> RERKRASKSSKHSMS.....	183
146	RLTRFHINQSELKDFGTEAAPQKGRKPRPRA.RSAKANQAELENAY	190